

#11

1600

RAW SEQUENCE LISTING

DATE: 10/05/2001

PATENT APPLICATION: US/09/674,817A

TIME: 13:55:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\10052001\I674817A.raw

3 <110> APPLICANT: Lorz, et al.

5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM
WHEAT AND

6 WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH

8 <130> FILE REFERENCE: 514413-3849

10 <140> CURRENT APPLICATION NUMBER: 09/674,817A

C--> 11 <141> CURRENT FILING DATE: 2001-11-06

13 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03141

14 <151> PRIOR FILING DATE: 1999-05-07

16 <150> PRIOR APPLICATION NUMBER: 19820608.9

17 <151> PRIOR FILING DATE: 1998-05-08

19 <160> NUMBER OF SEQ ID NOS: 10

21 <170> SOFTWARE: PatentIn version 3.0

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 2997

25 <212> TYPE: DNA

26 <213> ORGANISM: Triticum aestivum L. cv. Florida

28 <220> FEATURE:

29 <221> NAME/KEY: CDS

30 <222> LOCATION: (3)..(296)

31 <223> OTHER INFORMATION: exon 1

34 <220> FEATURE:

35 <221> NAME/KEY: CDS

36 <222> LOCATION: (2145)..(2921)

37 <223> OTHER INFORMATION: exon 3

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41 <221> NAME/KEY: Intron

42 <222> LOCATION: (297)..(396)

43 <223> OTHER INFORMATION: intron 1

46 <220> FEATURE:

47 <221> NAME/KEY: CDS

48 <222> LOCATION: (397)..(1617)

49 <223> OTHER INFORMATION: exon 2

52 <220> FEATURE:

53 <221> NAME/KEY: Intron

54 <222> LOCATION: (1618)..(2144)

55 <223> OTHER INFORMATION: intron 2

58 <400> SEQUENCE: 1

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60 Ser Gly Pro Ala Pro Arg Leu Arg Arg Trp Arg Pro Asn Ala Thr

61 1 5 10 15

63 gcg ggg aag ggg gtc ggc gag gtg tgc gcc gcg gtt gtc gag gcg gcg 95

64 Ala Gly Lys Gly Val Gly Glu Val Cys Ala Ala Val Val Glu Ala Ala

65 20 25 30

67 acg aag gta gag gac gag ggg gag gag gac gag ccg gtg gcg gag gac 143

68 Thr Lys Val Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp

69 35 40 45

71 agg tac gcg ctc ggc ggc gcg tgc agg gtg ctc gcc gga atg ccc gcg 191

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72 Arg Tyr Ala Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Ala
73      50      55      60
75 ccg ctg ggc gcc acc gcg ctc gcc ggc ggg gtc aat ttc gcc gtc tat      239
76 Pro Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr
77      65      70      75
79 tcc ggc gga gcc acc gcc gcg gcg ctc tgc ctc ttc acg cca gaa gat      287
80 Ser Gly Gly Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp
81 80      85      90      95
83 ctc aag gcg gtgggggttc ctcccgagta gagttcatca gctttgcgtg      336
84 Leu Lys Ala
87 cgccgcgcgc ccccttttttg ggccctgcaat ttaagttttg tactgggggca aatgctgcag      396
89 gat agg gtg acc gag gag gtt ccc ctt gac ccc ctg atg aat cgg acc      444
90 Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn Arg Thr
91      100      105      110
93 ggg aac gtg tgg cat gtc ttc atc gaa ggc gag ctg cac aac atg ctt      492
94 Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn Met Leu
95 115      120      125      130
97 tac ggg tac agg ttc gac ggc acc ttt gct cct cac tgc ggg cac tac      540
98 Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly His Tyr
99      135      140      145
101 ctt gat gtt tcc aat gtc gtg gtg gat cct tat gct aag gca gtg ata      588
102 Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala Val Ile
103      150      155      160
105 agc cga ggg gag tat ggt gtt cca gcg cgt ggt aac aat tgc tgg cct      636
106 Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys Trp Pro
107      165      170      175
109 cag atg gct ggc atg atc cct ctt cca tat agc acg ttt gat tgg gaa      684
110 Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp Trp Glu
111      180      185      190
113 ggc gac cta cct cta aga tat cct caa aag gac ctg gta ata tat gag      732
114 Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile Tyr Glu
115 195      200      205      210
117 atg cac ttg cgt gga ttc acg aag cat gat tca agc aat gta gaa cat      780
118 Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val Glu His
119      215      220      225
121 ccg ggt act ttc att gga gct gtg tgc aag ctt gac tat ttg aag gag      828
122 Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu Lys Glu
123      230      235      240
125 ctt gga gtt aat tgt att gaa tta atg ccc tgc cat gag ttc aac gag      876
126 Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe Asn Glu
127      245      250      255
129 ctg gag tac tca acc tct tct tcc aag atg aac ttt tgg gga tat tct      924
130 Leu Glu Tyr Ser Thr Ser Ser Ser Lys Met Asn Phe Trp Gly Tyr Ser
131      260      265      270
133 acc ata aac ttc ttt tca cca atg aca aga tac aca tca ggc ggg ata      972
134 Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly Gly Ile
135 275      280      285      290
137 aaa aac tgt ggg cgt gat gcc ata aat gag ttc aaa act ttt gta aga      1020
138 Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys Thr Phe Val Arg

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139		295		300		305		
141	gag gct cac	aaa cgg gga att	gag gtg atc ctg gat gtt gtc ttc aac	1068				
142	Glu Ala His	Lys Arg Gly Ile	Glu Val Ile Leu Asp Val Val Phe Asn					
143		310		315		320		
145	cat aca gct	gag ggt aat gag aat ggt cca ata tta tca ttt aag ggg	1116					
146	His Thr Ala	Glu Gly Asn Glu Asn Gly Pro Ile Leu Ser Phe Lys Gly						
147		325		330		335		
149	gtc gat aat act	aca tac tat atg ctt gca ccc aag gga gag ttt tat	1164					
150	Val Asp Asn Thr Thr Tyr Tyr Met Leu Ala Pro Lys Gly Glu Phe Tyr							
151		340		345		350		
153	aac tat tct ggc tgt ggg aat acc ttc aac tgt aat cat cct gtg gtt	1212						
154	Asn Tyr Ser Gly Cys Gly Asn Thr Phe Asn Cys Asn His Pro Val Val							
155	355		360		365		370	
157	cgt caa ttc att gta gat tgt tta aga tac tgg gtg acg gaa atg cat	1260						
158	Arg Gln Phe Ile Val Asp Cys Leu Arg Tyr Trp Val Thr Glu Met His							
159		375		380		385		
161	gtt gat ggt ttt cgt ttt gat ctt gca tcc ata atg acc aga ggt tcc	1308						
162	Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Ile Met Thr Arg Gly Ser							
163		390		395		400		
165	agt ctg tgg gat cca gtt aac gtg tat gga gct cca ata gaa ggt gac	1356						
166	Ser Leu Trp Asp Pro Val Asn Val Tyr Gly Ala Pro Ile Glu Gly Asp							
167		405		410		415		
169	atg atc aca aca ggg aca cct ctt gtt act cca cca ctt att gac atg	1404						
170	Met Ile Thr Thr Gly Thr Pro Leu Val Thr Pro Pro Leu Ile Asp Met							
171		420		425		430		
173	atc agc aat gac cca att ctt gga ggc gtc aag ctc att gct gaa gca	1452						
174	Ile Ser Asn Asp Pro Ile Leu Gly Gly Val Lys Leu Ile Ala Glu Ala							
175	435		440		445		450	
177	tgg gat gca gga ggc ctc tat caa gta ggt caa ttc cct cac tgg aat	1500						
178	Trp Asp Ala Gly Gly Leu Tyr Gln Val Gly Gln Phe Pro His Trp Asn							
179		455		460		465		
181	gtt tgg tct gag tgg aat ggg aag tac cgg gac att gtg cgt caa ttc	1548						
182	Val Trp Ser Glu Trp Asn Gly Lys Tyr Arg Asp Ile Val Arg Gln Phe							
183		470		475		480		
185	att aaa ggc act gat gga ttt gct ggt ggt ttt gcc gaa tgt ctt tgt	1596						
186	Ile Lys Gly Thr Asp Gly Phe Ala Gly Gly Phe Ala Glu Cys Leu Cys							
187		485		490		495		
189	gga agt cca cac cta tac cag gtaagtgtg gcaatacttg taaatgagtt	1647						
190	Gly Ser Pro His Leu Tyr Gln							
191		500		505				
193	gagtgaaatgt cacctggatt ttttatatat accacatgat gatacacatc taaatatata	1707						
195	acaatcatag tgtatgcata tgcatttggc taagaagtat tagtgtatac actagtgcata	1767						
197	tatatagggtt ttaacaccca acttgccaat gaaggaacat agggctttct agttatctta	1827						
199	tttatttgtc cgggtgaataa tccactgaaa aattccagcc atgtcatttt ttaggggggg	1887						
201	agaagaaact atattgattt gccccctaa aagaagccat ctcagaattc ataggtaagt	1947						
203	tgcttttctg taaagaaagg aaaacgactt catactttct atcggtgcta acttagctcg	2007						
205	atgtatatatt gtaagatgaa tgccaaattt aatttgcgg ataatttgat ctgtattca	2067						
207	caaatttcta tttggtttct ctagaaatca aaccagtaac ttgttattgg cactgcaact	2127						
209	tcttattgat taatcag gca gga gga agg aaa cct tgg cac agt atc aac	2177						

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210		Ala	Gly	Gly	Arg	Lys	Pro	Trp	His	Ser	Ile	Asn					
211						510					515						
213	ttt	gta	tgt	gca	cat	gat	gga	ttt	aca	ctg	gct	gat	ttg	gta	aca	tat	2225
214	Phe	Val	Cys	Ala	His	Asp	Gly	Phe	Thr	Leu	Ala	Asp	Leu	Val	Thr	Tyr	
215				520				525					530				
217	aat	aag	aag	tac	aat	tta	cca	aat	ggg	gag	aac	aac	aga	gat	gga	gaa	2273
218	Asn	Lys	Lys	Tyr	Asn	Leu	Pro	Asn	Gly	Glu	Asn	Asn	Arg	Asp	Gly	Glu	
219			535					540					545				
221	aat	cac	aat	ctt	agc	tgg	aat	tgt	ggg	gag	gaa	gga	gaa	ttc	gca	aga	2321
222	Asn	His	Asn	Leu	Ser	Trp	Asn	Cys	Gly	Glu	Glu	Gly	Glu	Phe	Ala	Arg	
223		550					555					560					
225	ttg	tct	gtc	aaa	aga	ttg	agg	aag	agg	cag	atg	cgc	aat	ttc	ttt	gtt	2369
226	Leu	Ser	Val	Lys	Arg	Leu	Arg	Lys	Arg	Gln	Met	Arg	Asn	Phe	Phe	Val	
227	565					570				575						580	
229	tgt	ctc	atg	gtt	tct	caa	gga	gtt	cca	atg	ttc	tac	atg	ggt	gat	gaa	2417
230	Cys	Leu	Met	Val	Ser	Gln	Gly	Val	Pro	Met	Phe	Tyr	Met	Gly	Asp	Glu	
231				585					590				595				
233	tat	ggc	cac	aca	aaa	ggg	ggc	aac	aac	aat	aca	tac	tgc	cat	gat	tct	2465
234	Tyr	Gly	His	Thr	Lys	Gly	Gly	Asn	Asn	Asn	Thr	Tyr	Cys	His	Asp	Ser	
235			600					605					610				
237	tat	gtc	aat	tat	ttt	cgc	tgg	gat	aaa	aaa	gaa	caa	tac	tct	gag	ttg	2513
238	Tyr	Val	Asn	Tyr	Phe	Arg	Trp	Asp	Lys	Lys	Glu	Gln	Tyr	Ser	Glu	Leu	
239		615					620					625					
241	cac	cga	ttc	tgc	tgc	ctc	atg	acc	aaa	ttc	cgc	aag	gag	tgc	gag	ggt	2561
242	His	Arg	Phe	Cys	Cys	Leu	Met	Thr	Lys	Phe	Arg	Lys	Glu	Cys	Glu	Gly	
243		630				635					640						
245	ctt	ggc	ctt	gag	gac	ttt	cca	acg	gcc	aaa	cgg	ctg	cag	tgg	cat	ggt	2609
246	Leu	Gly	Leu	Glu	Asp	Phe	Pro	Thr	Ala	Lys	Arg	Leu	Gln	Trp	His	Gly	
247	645				650				655							660	
249	cat	cag	cct	ggg	aag	cct	gat	tgg	tct	gag	aat	agc	cga	ttc	gtt	gcc	2657
250	His	Gln	Pro	Gly	Lys	Pro	Asp	Trp	Ser	Glu	Asn	Ser	Arg	Phe	Val	Ala	
251			665					670					675				
253	ttt	tcc	atg	aaa	gat	gaa	aga	cag	ggc	gag	atc	tat	gtg	gcc	ttc	aac	2705
254	Phe	Ser	Met	Lys	Asp	Glu	Arg	Gln	Gly	Glu	Ile	Tyr	Val	Ala	Phe	Asn	
255			680					685					690				
257	acc	agc	cac	tta	ccg	gcc	gtt	gtt	gag	ctc	cca	gag	cgc	gca	ggg	cgc	2753
258	Thr	Ser	His	Leu	Pro	Ala	Val	Val	Glu	Leu	Pro	Glu	Arg	Ala	Gly	Arg	
259		695					700					705					
261	cgg	tgg	gaa	ccg	gtg	gtg	gac	aca	ggc	aag	cca	gca	cca	tac	gac	ttc	2801
262	Arg	Trp	Glu	Pro	Val	Val	Asp	Thr	Gly	Lys	Pro	Ala	Pro	Tyr	Asp	Phe	
263		710				715					720						
265	ctc	acc	gac	gac	tta	cct	gat	cgc	gct	ctc	acc	ata	cac	cag	ttc	tcg	2849
266	Leu	Thr	Asp	Asp	Leu	Pro	Asp	Arg	Ala	Leu	Thr	Ile	His	Gln	Phe	Ser	
267	725				730				735							740	
269	cat	ttc	ctc	tac	tcc	aac	ctc	tac	ccc	atg	ctc	agc	tac	tca	tcg	gtc	2897
270	His	Phe	Leu	Tyr	Ser	Asn	Leu	Tyr	Pro	Met	Leu	Ser	Tyr	Ser	Ser	Val	
271			745					750					755				
273	atc	cta	gta	ttg	cgc	cct	gat	gtt	tgagagacca	atatatacag	taaataatat						2951
274	Ile	Leu	Val	Leu	Arg	Pro	Asp	Val									

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281 <211> LENGTH: 764
282 <212> TYPE: PRT
283 <213> ORGANISM: Triticum aestivum L. cv. Florida
285 <400> SEQUENCE: 2
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292          20          25          30
295 Lys Val Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp Arg
296          35          40          45
299 Tyr Ala Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Ala Pro
300          50          55          60
303 Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr Ser
304 65          70          75          80
307 Gly Gly Ala Thr Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp Leu
308          85          90          95
311 Lys Ala Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn
312          100         105         110
315 Arg Thr Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn
316          115         120         125
319 Met Leu Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly
320          130         135         140
323 His Tyr Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala
324 145         150         155         160
327 Val Ile Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys
328          165         170         175
331 Trp Pro Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp
332          180         185         190
335 Trp Glu Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile
336          195         200         205
339 Tyr Glu Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val
340          210         215         220
343 Glu His Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu
344 225         230         235         240
347 Lys Glu Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe
348          245         250         255
351 Asn Glu Leu Glu Tyr Ser Thr Ser Ser Ser Lys Met Asn Phe Trp Gly
352          260         265         270
355 Tyr Ser Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly
356          275         280         285
359 Gly Ile Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys Thr Phe
360          290         295         300
363 Val Arg Glu Ala His Lys Arg Gly Ile Glu Val Ile Leu Asp Val Val
364 305         310         315         320
367 Phe Asn His Thr Ala Glu Gly Asn Glu Asn Gly Pro Ile Leu Ser Phe
368          325         330         335

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VERIFICATION SUMMARY

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